## SEQUENCE LISTING

- <110> McCall, Catherine A. Hunter, Shirley Wu Weber, Eric R.
- <120> NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS AND USES THEREOF
- <130> AL-2-C4
- <140> not yet assigned
- <141> 2000-09-14
- <150> 09/292,225
- <151> 1999-04-15
- <150> 60/098,909
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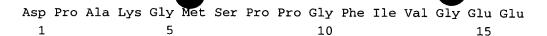
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	cca Pro														-	960
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	tac Tyr		-						_				_	-		1056
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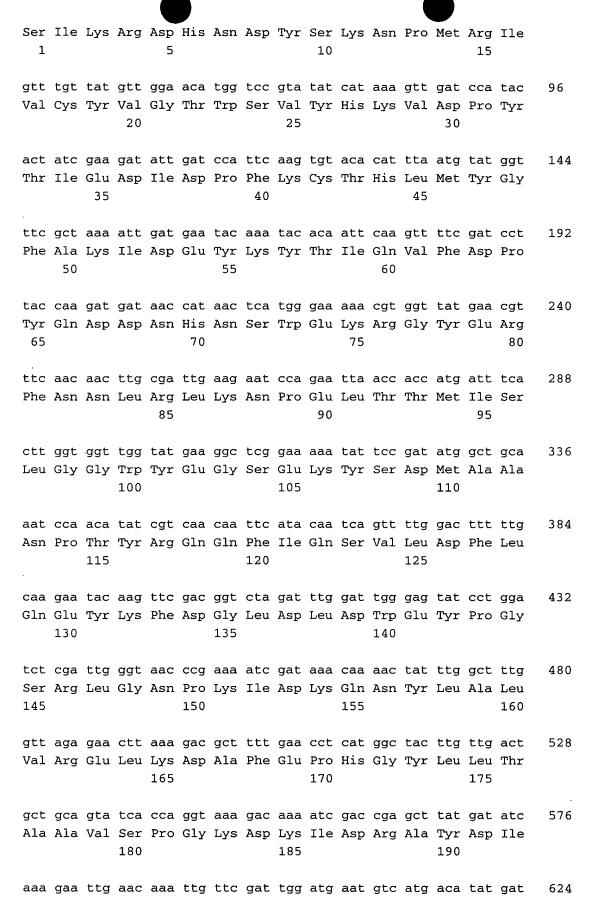
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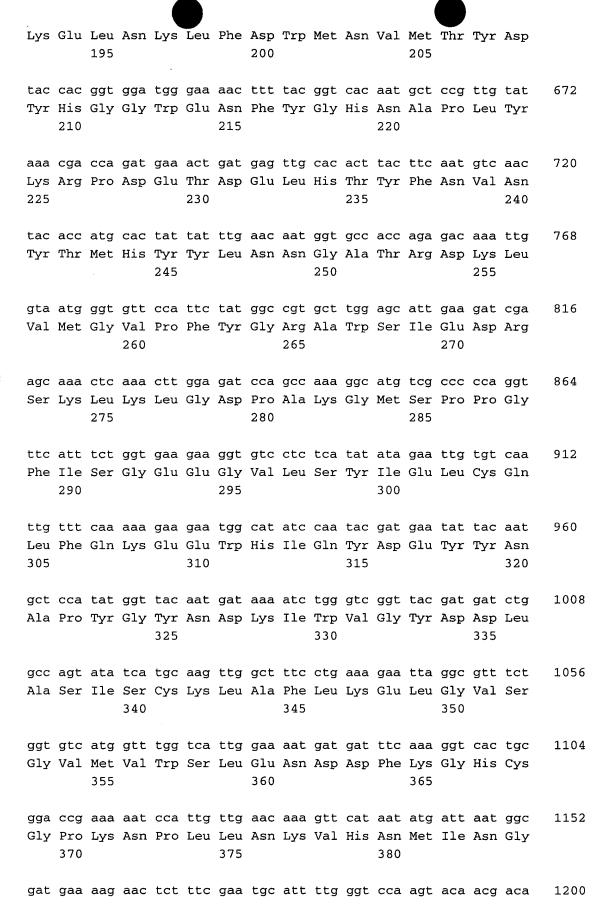
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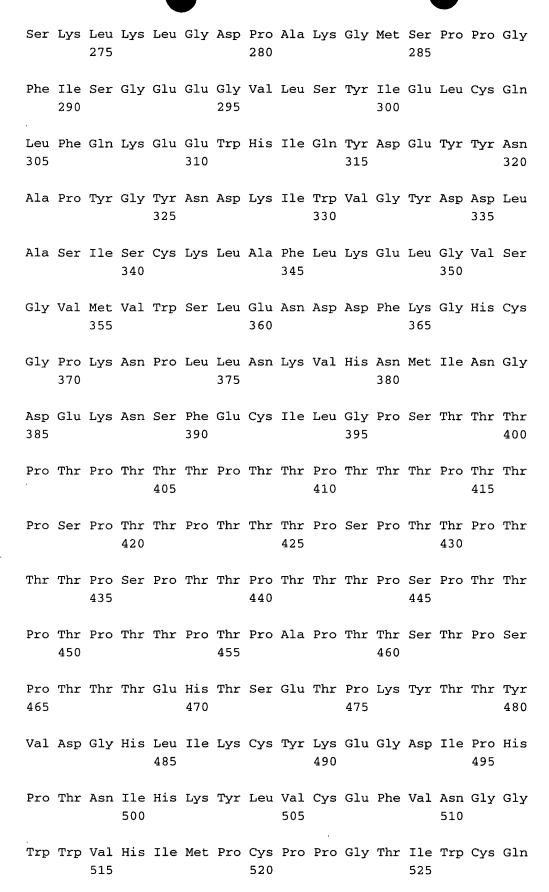
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<210> 23

<211> 25

<212> PRT

<213> Dermatophagoides farinae

<220>

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     <220>
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Ser Ile Lys Arg Asp His Asn Asp Tyr Ser Lys Asn Pro Met Met Ile
ı
      1
                       5
m
1
    Val Xaa Tyr Gly Gly Ser Ser Gly Tyr Gln Ser Xaa Lys Arg Xaa Xaa
20
                                      25
                                                          30
    Thr
Ħ
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<212> DNA

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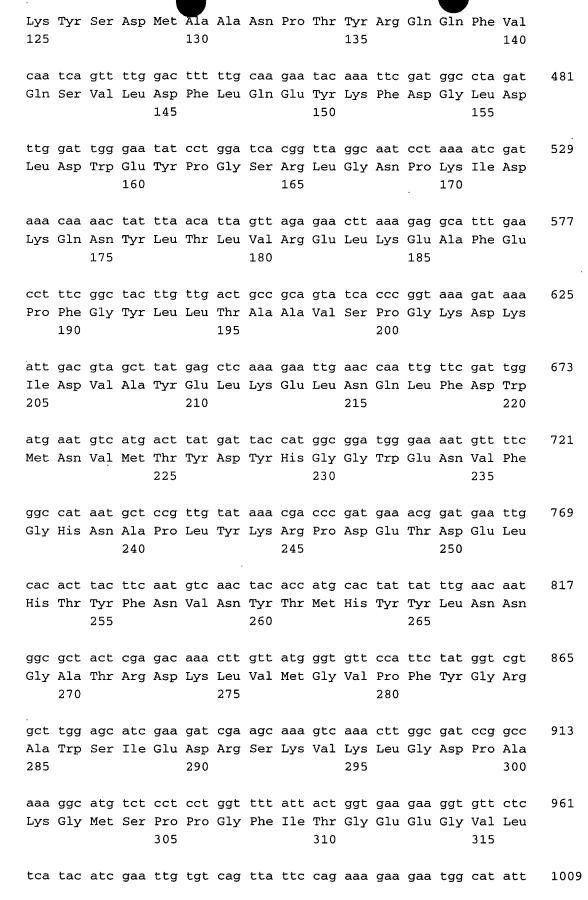
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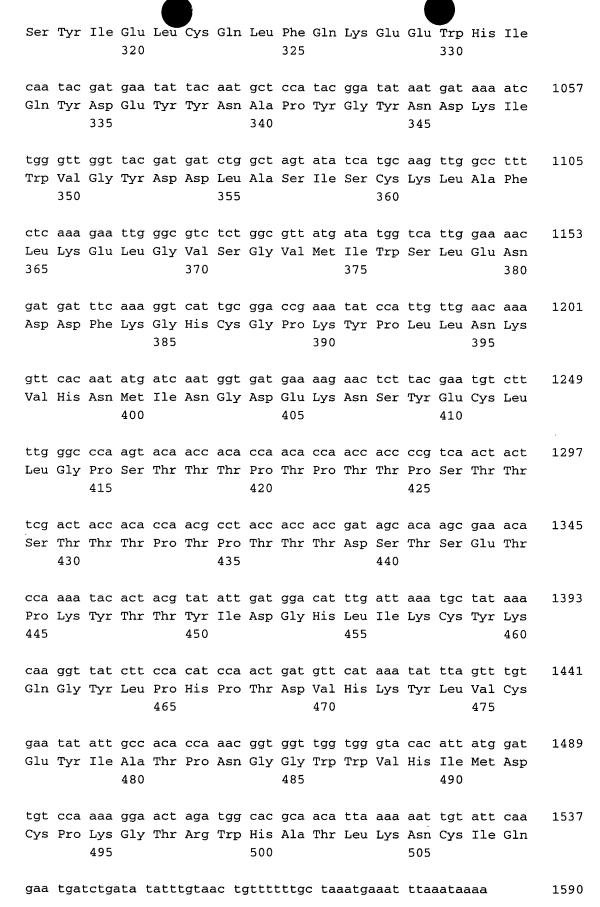
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10

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		3> De		opha	agoid	des i	farin	nae									
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					_				5					10			
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	Cys	Ile	Gly 15	Leu	Met	Asn	Ala	Ala 20	Thr	Lys	Arg	Asp	His 25	Asn	Asn	Tyr	
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	Ser	Lys 30	Asn	Pro	Met	Arg	Ile 35	Val	Cys	Tyr	Val	Gly 40	Thr	Trp	Ser	Val	
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_ ]	Tyr	His	Lys	Val	Asp	Pro	Tyr	Thr	Ile	Glu	Asp	Ile	Asp	Pro	Phe	Lys	
	45					50					55					60	
]	tgt	act	cat	ttg	atg	tat	ggt	ttt	gct	aaa	atc	gat	gaa	tac	aaa	tac	241
J	Суѕ	Thr	His	Leu	Met 65	Tyr	Gly	Phe	Ala	Lys 70	Ile	Asp	Glu	Tyr	Lys 75	Tyr	
	acc	att	caa	gtt	ttt	gat	cca	ttt	caa	gat	gat	aac	cat	aac	tca	tgg	289
	Thr	Ile	Gln	Val 80	Phe	Asp	Pro	Phe	Gln 85	Asp	Asp	Asn	His	Asn 90	Ser	Trp	
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												Arg					
			95					100					105				
	gaa	ttg	acc	acc	atg	att	tca	ttg	ggt	ggt	tgg	tat	gaa	ggt	tca	gaa	385
	Glu	Leu 110	Thr	Thr	Met	Ile	Ser 115	Leu	Gly	Gly	Trp	Туr 120	Glu	Gly	Ser	Glu	
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Asp Pro Tyr Thr Ile Glu Asp Ile Asp Pro Phe Lys Cys Thr His Leu 50 55 60

Met Tyr Gly Phe Ala Lys Ile Asp Glu Tyr Lys Tyr Thr Ile Gln Val 65 70 75 80

Phe Asp Pro Phe Gln Asp Asp Asn His Asn Ser Trp Glu Lys His Gly 85 90 95

Tyr Glu Arg Phe Asn Asn Leu Arg Leu Lys Asn Pro Glu Leu Thr Thr
100 105 110

Met Ile Ser Leu Gly Gly Trp Tyr Glu Gly Ser Glu Lys Tyr Ser Asp 115 120 125

Met Ala Ala Asn Pro Thr Tyr Arg Gln Gln Phe Val Gln Ser Val Leu 130 135 140

Asp Phe Leu Gln Glu Tyr Lys Phe Asp Gly Leu Asp Leu Asp Trp Glu 145 150 155 160

Tyr Pro Gly Ser Arg Leu Gly Asn Pro Lys Ile Asp Lys Gln Asn Tyr 165 170 175

Leu Thr Leu Val Arg Glu Leu Lys Glu Ala Phe Glu Pro Phe Gly Tyr 180 185 190

Leu Leu Thr Ala Ala Val Ser Pro Gly Lys Asp Lys Ile Asp Val Ala

195 200 205

Tyr	Glu 210	Leu	Lys	Glu	Leu	Asn 215	Gln	Leu	Phe	Asp	Trp 220	Met	Asn	Val	Met
Thr 225	Tyr	Asp	Tyr	His	Gly 230	Gly	Trp	Glu	Asn	Val 235	Phe	Gly	His	Asn	Ala 240
Pro	Leu	Tyr	Lys	Arg 245	Pro	Asp	Glu	Thr	Asp 250	Glu	Leu	His	Thr	Tyr 255	Phe
Asn	Val	Asn	Tyr 260	Thr	Met	His	Tyr	Tyr 265	Leu	Asn	Asn	Gly	Ala 270	Thr	Arg
Asp	Lys	Leu 275	Val	Met	Gly	Val	Pro 280	Phe	Tyr	Gly	Arg	Ala 285	Trp	Ser	Ile
Glu	Asp 290	Arg	Ser	Lys	Val	Lys 295	Leu	Gly	Asp	Pro	Ala 300	Lys	Gly	Met	Ser
Pro 305	Pro	Gly	Phe	Ile	Thr 310	Gly	Glu	Glu	Gly	Val 315	Leu	Ser	Tyr	Ile	Glu 320
Leu	Cys	Gln	Leu	Phe 325	Gln	Lys	Glu	Glu	Trp 330	His	Ile	Gln	Tyr	Asp 335	Glu
Tyr	Tyr	Asn	Ala 340	Pro	Tyr	Gly	Tyr	Asn 345	Asp	Lys	Ile	Trp	Val 350	Gly	Tyr
Asp	Asp	Leu 355	Ala	Ser	Ile	Ser	Cys 360	Lys	Leu	Ala	Phe	Leu 365	Lys	Glu	Leu
Gly	Val 370	Ser	Gly	Val	Met	Ile 375	Trp	Ser	Leu	Glu	Asn 380	Asp	Asp	Phe	Lys
Gly 385	His	Cys	Gly	Pro	Lys 390	Tyr	Pro	Leu	Leu	Asn 395	Lys	Val	His	Asn	Met 400
Ile	Asn	Gly	Asp	Glu 405	Lys	Asn	Ser	Tyr	Glu 410	Cys	Leu	Leu	Gly	Pro 415	Ser
Thr	Thr	Thr	Pro 420	Thr	Pro	Thr	Thr	Pro 425	Ser	Thr	Thr	Ser	Thr 430	Thr	Thr
Pro	Thr	Pro 435	Thr	Thr	Thr	Asp	Ser 440	Thr	Ser	Glu	Thr	Pro 445	Lys	Tyr	Thr
Thr	Tyr	Ile	Asp	Gly	His	Leu	Ile	Lys	Cys	Tyr	Lys	Gln	Gly	Tyr	Leu

450 455 460

Pro His Pro Thr Asp Val His Lys Tyr Leu Val Cys Glu Tyr Ile Ala 465 470 475 480

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485 490 495

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<210> 36

<211> 1621

<212> DNA

<213> Dermatophagoides farinae

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	2> DI 3> De	NA ermat	copha	agoio	des :	farin	nae									
	l> CI	os 1)	(1527	7)												
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_		gcg Ala	_			_	_					_				96
		atc Ile 35													_	144
		tac Tyr				_		-				_			_	192
		ggt Gly													-	240
		cca Pro										-				288
		cgt Arg										_	_			336
		tca Ser 115												_	_	384
		gcc Ala												-	_	432
gac	ttt	ttg	caa	gaa	tac	aaa	ttc	gat	ggc	cta	gat	ttg	gat	tgg	gaa	480

Asp 145	Phe	Leu	Gln	Glu	Tyr 150	Lys	Phe	Asp	Gly	Leu 155	Asp	Leu	Asp	Trp	Glu 160	
					tta Leu						-					528
			-	_	gaa Glu				-		-					576
-	_		_	_	gta Val					-			_	_	-	624
				-	ttg Leu			_		_		-		-	•	672
		_			ggc Gly 230			_		-					-	720
_	_			-	ccc Pro	-	<b>-</b>		_	- T	_					768
	-				atg Met				_				_		~	816
_			_	_	ggt Gly	•					_	_		-		864
		_	_		gtc Val				_	-	_			_		912
					act Thr 310		_	_		_					-	960
	-	_			cag Gln		_	_						-	_	1008
tat	tac	aat	gct	cca	tac	gga	tat	aat	gat	aaa	atc	tgg	gtt	ggt	tac	1056



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	Asp	Asp		Ala	Ser	Ile	Ser		Lys	Leu	Ala	Phe		Lys	Glu	Leu	
			355					360					365				
	ggc	gtc	tct	ggc	gtt	atg	ata	tgg	tca	ttg	gaa	aac	gat	gat	ttc	aaa	1152
	Gly		Ser	Gly	Val	Met		Trp	Ser	Leu	Glu	Asn	Asp	Asp	Phe	Lys	
		370					375					380					
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	Gly	His	Cys	${\tt Gly}$	Pro	Lys	Tyr	Pro	Leu	Leu	Asn	Lys	Val	His	Asn	Met	
	385					390					395					400	
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	Ile	Asn	Gly	Asp	Glu	Lys	Asn	Ser	Tyr	Glu	Cys	Leu	Leu	Gly	Pro	Ser	
					405					410					415		
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						Pro			-				_				
				420					425					430			
	cca	acg	cct	acc	acc	acc	gat	agc	aca	agc	gaa	aca	cca	aaa	tac	act	1344
	Pro	Thr		Thr	Thr	Thr	Asp	Ser	Thr	Ser	Glu	Thr	Pro	Lys	Tyr	Thr	
Ų			435					440					445				
	acg	tat	att	gat	gga	cat	ttg	att	aaa	tgc	tat	aaa	caa	ggt	tat	ctt	1392
	Thr		Ile	Asp	Gly	His		Ile	Lys	Суѕ	Tyr		Gln	Gly	Tyr	Leu	
		450					455					460					
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3	Pro	His	Pro	Thr	Asp	Val	His	Lys	Tyr	Leu	Val	Cys	Glu	Tyr	Ile	Ala	
	465					470					475					480	
	aca	cca	aac	ggt	ggt	tgg	tgg	gta	cac	att	atg	gat	tgt	cca	aaa	gga	1488
	Thr	Pro	Asn	Gly	Gly	Trp	Trp	Val	His	Ile	Met	Asp	Cys	Pro	Lys	Gly	
					485					490					495		
	act	aga	tgg	cac	gca	aca	tta	aaa	aat	tgt	att	caa	gaa				1527
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<213> Dermatophagoides farinae

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Phe Asp Pro Phe Gln Asp Asp Asn His Asn Ser Trp Glu Lys His Gly
85 90 95

Tyr Glu Arg Phe Asn Asn Leu Arg Leu Lys Asn Pro Glu Leu Thr Thr
100 105 110

Met Ile Ser Leu Gly Gly Trp Tyr Glu Gly Ser Glu Lys Tyr Ser Asp 115 120 125

Met Ala Ala Asn Pro Thr Tyr Arg Gln Gln Phe Val Gln Ser Val Leu 130 135 140

Asp Phe Leu Gln Glu Tyr Lys Phe Asp Gly Leu Asp Leu Asp Trp Glu 145 150 155 160

Tyr Pro Gly Ser Arg Leu Gly Asn Pro Lys Ile Asp Lys Gln Asn Tyr 165 170 175

Leu Thr Leu Val Arg Glu Leu Lys Glu Ala Phe Glu Pro Phe Gly Tyr 180 185 190

Leu Leu Thr Ala Ala Val Ser Pro Gly Lys Asp Lys Ile Asp Val Ala 195 200 205

Tyr Glu Leu Lys Glu Leu Asn Gln Leu Phe Asp Trp Met Asn Val Met 210 215 220

Thr Tyr Asp Tyr His Gly Gly Trp Glu Asn Val Phe Gly His Asn Ala 225 230 235 240

Pro Leu Tyr Lys Arg Pro Asp Glu Thr Asp Glu Leu His Thr Tyr Phe

245 250 255

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Glu	Asp 290	Arg	Ser	Lys	Val	Lys 295	Leu	Gly	Asp	Pro	Ala 300	Lys	Gly	Met	Ser

- Pro Pro Gly Phe Ile Thr Gly Glu Glu Gly Val Leu Ser Tyr Ile Glu 305 310 315 320
- Leu Cys Gln Leu Phe Gln Lys Glu Glu Trp His Ile Gln Tyr Asp Glu 325 330 335
- Tyr Tyr Asn Ala Pro Tyr Gly Tyr Asn Asp Lys Ile Trp Val Gly Tyr 340 345 350
- Asp Asp Leu Ala Ser Ile Ser Cys Lys Leu Ala Phe Leu Lys Glu Leu 355 360 365
- Gly Val Ser Gly Val Met Ile Trp Ser Leu Glu Asn Asp Asp Phe Lys 370 380
- Gly His Cys Gly Pro Lys Tyr Pro Leu Leu Asn Lys Val His Asn Met 385 390 395 400
- Ile Asn Gly Asp Glu Lys Asn Ser Tyr Glu Cys Leu Leu Gly Pro Ser 405 410 415
- Thr Thr Thr Pro Thr Pro Thr Thr Pro Ser Thr Thr Ser Thr Thr Thr 420 425 430
- Pro Thr Pro Thr Thr Thr Asp Ser Thr Ser Glu Thr Pro Lys Tyr Thr
  435 440 445
- Thr Tyr Ile Asp Gly His Leu Ile Lys Cys Tyr Lys Gln Gly Tyr Leu 450 455 460
- Pro His Pro Thr Asp Val His Lys Tyr Leu Val Cys Glu Tyr Ile Ala 465 470 475 480
- Thr Pro Asn Gly Gly Trp Trp Val His Ile Met Asp Cys Pro Lys Gly
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	gat Asp							_	_	240
	aac Asn									288
	ggt Gly								_	336
	aca Thr 115						-		-	384
	tac Tyr									432
	tta Leu									480
	gaa Glu							-		528
	gta Val									576

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											_	_		tat Tyr	_	624
												-	_	ttg Leu		672
	_		_	_	_	_	_	_						gtc Val		720
										_		_	_	aaa Lys 255		768
-	_		~					~	-		~		-	gat Asp	- 3 -	816
-		_				_	_	-			_			cct Pro		864
				_	_		_					_	_	tgt Cys	-	912
		_		-	_						•	_		tac Tyr		960
														gat Asp 335		1008
	_			-	_	_	-				-	_		gtc Val		1056
	-	_				_	•		_	_				cat His	_	1104
	_				-	_			-			_		aat Asn		1152

				(										)		
	gaa Glu											-				1200
	aca Thr				_				_					_		1248
	acc Thr												_			1296
	gga Gly															1344
	gat Asp 450	-					-	_	_			_				1392
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Thr	Ile	Glu 35	Asp	Ile	Asp	Pro	Phe 40	Lys	Cys	Thr	His	Leu 45	Met	Tyr	Gly	
Phe	Ala 50	Lys	Ile	Asp	Glu	Tyr 55	Lys	Tyr	Thr	Ile	Gln 60	Val	Phe	Asp	Pro	

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Phe Asn Asn Leu Arg Leu Lys Asn Pro Glu Leu Thr Thr Met Ile Ser
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Leu Gly Gly Trp Tyr Glu Gly Ser Glu Lys Tyr Ser Asp Met Ala Ala 100 105 110

Asn Pro Thr Tyr Arg Gln Gln Phe Val Gln Ser Val Leu Asp Phe Leu 115 120 125

Gln Glu Tyr Lys Phe Asp Gly Leu Asp Leu Asp Trp Glu Tyr Pro Gly 130 135 140

Ser Arg Leu Gly Asn Pro Lys Ile Asp Lys Gln Asn Tyr Leu Thr Leu 145 150 155 160

Val Arg Glu Leu Lys Glu Ala Phe Glu Pro Phe Gly Tyr Leu Leu Thr 165 170 175

Ala Ala Val Ser Pro Gly Lys Asp Lys Ile Asp Val Ala Tyr Glu Leu 180 185 190

Lys Glu Leu Asn Gln Leu Phe Asp Trp Met Asn Val Met Thr Tyr Asp 195 200 205

Tyr His Gly Gly Trp Glu Asn Val Phe Gly His Asn Ala Pro Leu Tyr 210 215 220

Lys Arg Pro Asp Glu Thr Asp Glu Leu His Thr Tyr Phe Asn Val Asn 225 230 235 240

Tyr Thr Met His Tyr Tyr Leu Asn Asn Gly Ala Thr Arg Asp Lys Leu 245 250 255

Val Met Gly Val Pro Phe Tyr Gly Arg Ala Trp Ser Ile Glu Asp Arg 260 265 270

Ser Lys Val Lys Leu Gly Asp Pro Ala Lys Gly Met Ser Pro Pro Gly 275 280 285

Phe Ile Thr Gly Glu Glu Gly Val Leu Ser Tyr Ile Glu Leu Cys Gln
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Leu Phe Gln Lys Glu Glu Trp His Ile Gln Tyr Asp Glu Tyr Tyr Asn 305 310 315 320

Ala Pro Tyr Gly Tyr Asn Asp Lys Ile Trp Val Gly Tyr Asp Asp Leu

325 330 335

Ala Ser Ile Ser Cys Lys Leu Ala Phe Leu Lys Glu Leu Gly Val Ser 340 345 350

Gly Val Met Ile Trp Ser Leu Glu Asn Asp Asp Phe Lys Gly His Cys 355 360 365

Gly Pro Lys Tyr Pro Leu Leu Asn Lys Val His Asn Met Ile Asn Gly 370 380

Asp Glu Lys Asn Ser Tyr Glu Cys Leu Leu Gly Pro Ser Thr Thr Thr 385 390 395 400

Pro Thr Pro Thr Thr Pro Ser Thr Thr Ser Thr Thr Thr Pro Thr Pro 405 410 415

Thr Thr Thr Asp Ser Thr Ser Glu Thr Pro Lys Tyr Thr Thr Tyr Ile
420 425 430

Asp Gly His Leu Ile Lys Cys Tyr Lys Gln Gly Tyr Leu Pro His Pro 435 440 445

Thr Asp Val His Lys Tyr Leu Val Cys Glu Tyr Ile Ala Thr Pro Asn 450 455 460

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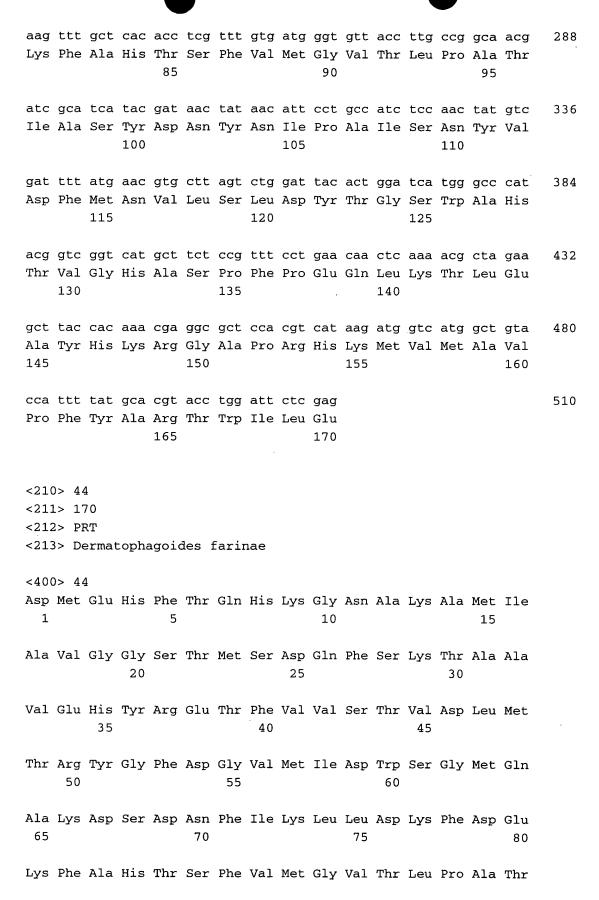
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                                                                    96
Ala Val Gly Gly Ser Thr Met Ser Asp Gln Phe Ser Lys Thr Ala Ala
             20
                                  25
                                                      30
gta gaa cat tat cgg gaa acg ttt gtt gtt agc aca gtt gat ctt atg
                                                                    144
Val Glu His Tyr Arg Glu Thr Phe Val Val Ser Thr Val Asp Leu Met
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                              40
                                                  45
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Thr Arg Tyr Gly Phe Asp Gly Val Met Ile Asp Trp Ser Gly Met Gln
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                         55
                                              60
gcc aaa gat agt gat aat ttc att aaa ttg ttg gac aaa ttc gac gaa
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Ala Lys Asp Ser Asp Asn Phe Ile Lys Leu Leu Asp Lys Phe Asp Glu
 65
                     70
                                          75
                                                               80
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90 95

Ile Ala Ser Tyr Asp Asn Tyr Asn Ile Pro Ala Ile Ser Asn Tyr Val 100 105 110

Asp Phe Met Asn Val Leu Ser Leu Asp Tyr Thr Gly Ser Trp Ala His
115 120 125

Thr Val Gly His Ala Ser Pro Phe Pro Glu Gln Leu Lys Thr Leu Glu 130 135 140

Ala Tyr His Lys Arg Gly Ala Pro Arg His Lys Met Val Met Ala Val 145 150 155 160

Pro Phe Tyr Ala Arg Thr Trp Ile Leu Glu 165 170

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<211> 510

<212> DNA

<213> Dermatophagoides farinae

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Primer

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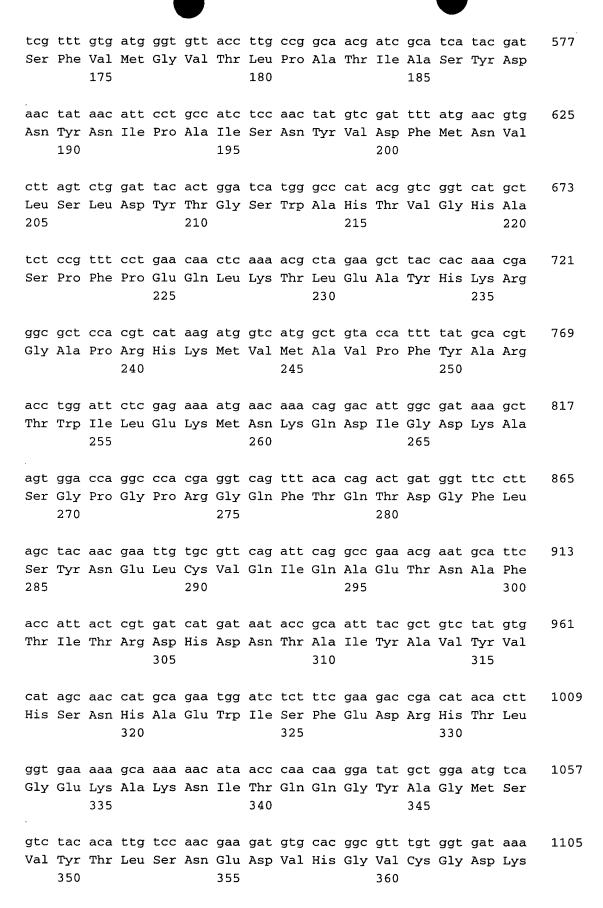
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165

170

160



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	gaa Glu														gaa Glu	1201
	gtg Val		-							_		_	_			1249
	cgc Arg	_	_			_	_				-	-				1297
	ttt Phe 430									-					_	1345
	ttt Phe	_	_	_	_			-		_						1393
	tgt Cys	tgaa	ataca	aaa t	caaaa	attad	ca at	ccact	ttaa	a aaa	aaaa	aaaa	aaaa	aaa		1445
	- 4															
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Cys	Tyr	Tyr 35	Glu	Ser	Trp	Val	His 40	Trp	Arg	Gln	Gly	Glu 45	Gly	Lys	Met	
Asp	Pro 50	Glu	Asp	Ile	Asp	Thr 55	Ser	Leu	Суѕ	Thr	His 60	Ile	Val	Tyr	Ser	

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65 70 75 80

Tyr Leu Met Lys Asp Leu His Asp Met Glu His Phe Thr Gln His Lys

85 90 95

Gly Asn Ala Lys Ala Met Ile Ala Val Gly Gly Ser Thr Met Ser Asp 100 105 110

Gln Phe Ser Lys Thr Ala Ala Val Glu His Tyr Arg Glu Thr Phe Val 115 120 125

Val Ser Thr Val Asp Leu Met Thr Arg Tyr Gly Phe Asp Gly Val Met 130 135 140

Ile Asp Trp Ser Gly Met Gln Ala Lys Asp Ser Asp Asn Phe Ile Lys
145 150 155 160

Leu Leu Asp Lys Phe Asp Glu Lys Phe Ala His Thr Ser Phe Val Met
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Gly Val Thr Leu Pro Ala Thr Ile Ala Ser Tyr Asp Asn Tyr Asn Ile 180 185 190

Pro Ala Ile Ser Asn Tyr Val Asp Phe Met Asn Val Leu Ser Leu Asp 195 200 205

Tyr Thr Gly Ser Trp Ala His Thr Val Gly His Ala Ser Pro Phe Pro 210 215 220

Glu Gln Leu Lys Thr Leu Glu Ala Tyr His Lys Arg Gly Ala Pro Arg 225 230 235 240

His Lys Met Val Met Ala Val Pro Phe Tyr Ala Arg Thr Trp Ile Leu 245 250 255

Glu Lys Met Asn Lys Gln Asp Ile Gly Asp Lys Ala Ser Gly Pro Gly
260 265 270

Pro Arg Gly Gln Phe Thr Gln Thr Asp Gly Phe Leu Ser Tyr Asn Glu 275 280 285

Leu Cys Val Gln Ile Gln Ala Glu Thr Asn Ala Phe Thr Ile Thr Arg
290 295 300

Asp His Asp Asn Thr Ala Ile Tyr Ala Val Tyr Val His Ser Asn His 305 310 315 320

Ala Glu Trp Ile Ser Phe Glu Asp Arg His Thr Leu Gly Glu Lys Ala

325 330 335

Lys Asn Ile Thr Gln Gln Gly Tyr Ala Gly Met Ser Val Tyr Thr Leu  $340 \hspace{1cm} 345 \hspace{1cm} 350$ 

Ser Asn Glu Asp Val His Gly Val Cys Gly Asp Lys Asn Pro Leu Leu 355 360 365

His Ala Ile Gln Ser Asn Tyr Tyr His Gly Val Val Thr Glu Pro Thr 370 375 380

Val Val Thr Leu Pro Pro Val Thr His Thr Thr Glu His Val Thr Asp 385 390 395 400

Ile Pro Gly Val Phe His Cys His Glu Glu Gly Phe Phe Arg Asp Lys
405
410
415

Thr Tyr Cys Ala Thr Tyr Tyr Glu Cys Lys Lys Gly Asp Phe Gly Leu 420 425 430

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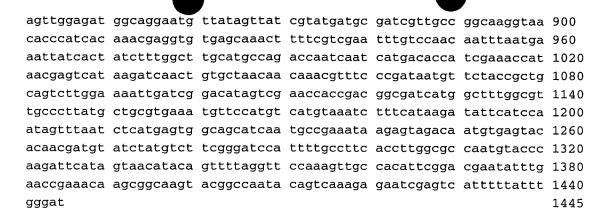
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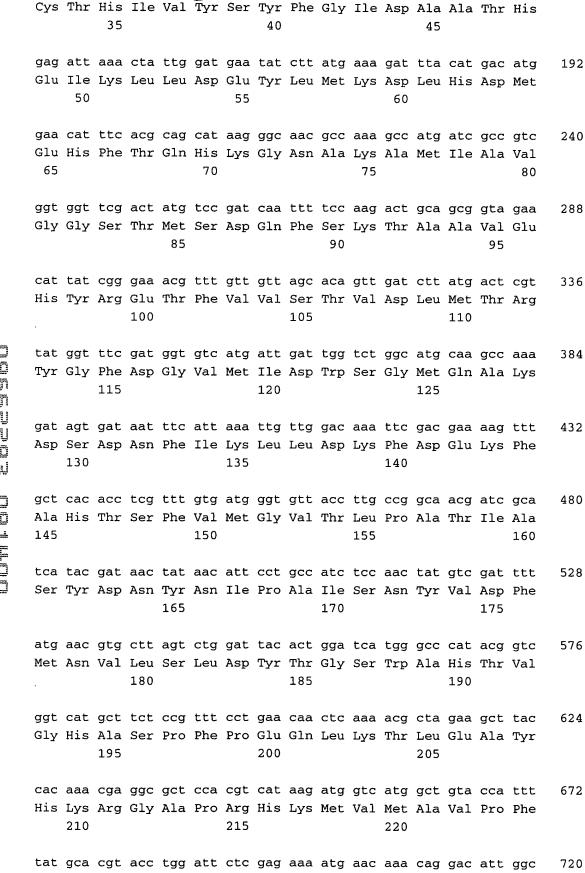
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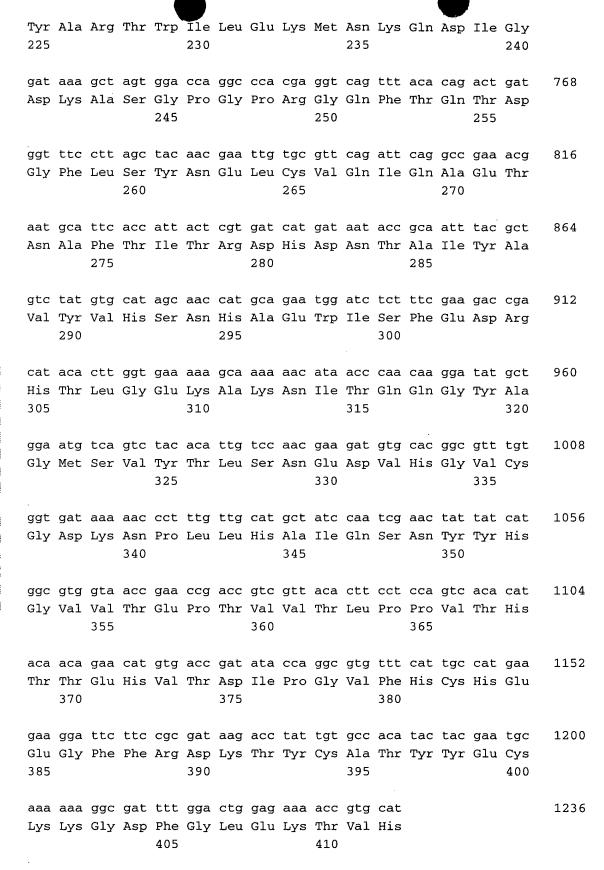
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## <213> Dermatophagoides farinae

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                  5
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                                                         15
cgc caa ggt gaa ggc aaa atg gat ccc gaa gac ata gat aca tcg ttg
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Arg Gln Gly Glu Gly Lys Met Asp Pro Glu Asp Ile Asp Thr Ser Leu
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Tyr Ala Arg Thr Trp Ile Leu Glu Lys Met Asn Lys Gln Asp Ile Gly
225 230 235 240

Asp Lys Ala Ser Gly Pro Gly Pro Arg Gly Gln Phe Thr Gln Thr Asp 245 250 255

Gly Phe Leu Ser Tyr Asn Glu Leu Cys Val Gln Ile Gln Ala Glu Thr 260 265 270

Asn Ala Phe Thr Ile Thr Arg Asp His Asp Asn Thr Ala Ile Tyr Ala 275 280 285

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His Thr Leu Gly Glu Lys Ala Lys Asn Ile Thr Gln Gln Gly Tyr Ala 305 310 315 320

Gly Met Ser Val Tyr Thr Leu Ser Asn Glu Asp Val His Gly Val Cys 325 330 335

Gly Asp Lys Asn Pro Leu Leu His Ala Ile Gln Ser Asn Tyr Tyr His 340 345 350

Gly Val Val Thr Glu Pro Thr Val Val Thr Leu Pro Pro Val Thr His 355 360 365

Thr Thr Glu His Val Thr Asp Ile Pro Gly Val Phe His Cys His Glu 370 375 380

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